

## GENETIC DIVERSITY STUDY OF ELITE RICE GENOTYPES FOR SEED AND SEEDLING TRAITS

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### ABSTRACT

Healthy seedling is the source of a healthy plant and ultimately high yield. Different seed traits affected seedling development in different ways. An experiment comprising thirty-five genotypes of rice was conducted for assessing the effect of different seed and seed vigour traits on seedling development. Data on nine seed and seedling traits viz. 1000 seed weight, seed length, seed breadth, l/b ratio, germination, seedling length radical length, plumule length and radical plumule ratio was recorded and statistically analysed for variance, mean performance, genetic variability, heritability and  $D^2$  statistics analysis. High values of genotypic coefficient of variation and phenotypic coefficient of variation were observed for radical plumule ratio followed by plumule length, and radical length. High heritability coupled with a high genetic advance was recorded for seedling length, radical length and plumule length. Analysis of Mahalanobis  $D^2$  revealed that considerable amount of diversity existed in the material. The 35 genotypes were grouped in to six clusters, among these clusters; cluster II had maximum number of genotypes 14. The intra-cluster distance varied from 21385.84 for cluster II to 39890.34 for cluster IV and the inter-cluster distance varied from 23918.1 between cluster I and I to (480157.200) between cluster VI and I. The highest cluster mean has been observed for 1000 seed weight and seed length for cluster VI, seed length and L/B ratio from cluster III, germination percentage and plumule length, for cluster I, seedling length and radical length for cluster V and radical plumule ratio for cluster II. Seedling length exhibited the maximum contribution to total genetic divergence (58.99%), followed by radical length (25.04%) and plumule length (15.97%) while as other remaining traits contributed little towards genetic divergence. All the descriptors in this study showed that there is ample of genetic diversity present among genotypes and this information can be useful for breeder to choose right parents for crop improvement.

**KEYWORDS:** Rice, Genetic Variability,  $D_2$  Analysis

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### INTRODUCTION

Rice is the premier food crop in the world and it feeds about half of the world population and occupies almost one-fifth of the total land area covered under cereals (Vaughan *et al.*, 2003) and it ranks next to wheat (Bashir *et al.*, 2010). There is an increased demand of rice due to growing population, hence, in order to meet the world's rice requirements there is a need to develop varieties with potential of high yield and resistance against biotic and abiotic stresses. High quality seed is the key to successful agriculture. Present agriculture is transforming to the use of technology and précised use of inputs, which stress upon the use of healthy seed for good germination and a vigorous seedling to ensure a high yield. Uniformity of growth and synchrony in development is highly desirable characters for mechanized cultural operations. As such, only of high quality i.e., genetically pure and morphologically, pathologically and physiologically sound seed is capable of increasing the

productivity, the seeds should also have better storability to produce good crop during the next season. Genetic diversity represents the heritable variation within and between populations. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits, and efficient selection strategies that make it possible to exploit existing genetic resource. The pool of genetic variation within a random mating population is the basis for selection as well as for plant improvement. Genetic distance within different genotypes in a population can be estimated by different methods as it is crucial to understand the usable variability existing in them. Multivariate analysis is one of such approach for understanding the variability and diversity. Knowledge about heritability helps plant breeders to predict the genetic behaviour of the later generations and for genetic improvement through selection. Assessment of genetic diversity is an integral part of crop improvement as exploitation of the genetic diversity helps the plant breeder to develop new varieties (Manonmani and Khan, 2003)

## MATERIALS AND METHODS

The present experiment was carried out during 2014 at department of Plant Breeding and Genetics SKUAST-K, Khudwani, Anantnag, Kashmir. The experimental material for present study comprised of thirty five released and advanced lines of rice (*Oryza sativa* L.). These genotypes were developed and maintained at SKUAST-K, Khudwani, Anantnag.

The experiment was laid in replicate of three set and data on seed, seedling and related traits were recorded from ten randomly selected plants of each genotype. The Standard Evaluation System for Rice of IRRI (Anonymous, 1996) was followed for recording observation for each of the character viz. 1000 seed weight (g), seed length (mm), seed breadth (mm), length breadth ratio, germination percentage, seedling length (cm), root length (cm), shoot length (cm), root shoot ratio.

**Length Breadth Ratio:** Length breadth ratio was worked out by using the following formula

$$L/B \text{ ratio} = \text{mean length of the seed (mm)} / \text{mean breadth of the seed (mm)}$$

## Germination

Germination test was conducted by adopting blotting paper method as described by ISTA procedures (Anonymous, 1999).

$$\text{Germination (\%)} = \frac{\text{Number of seeds germinated}}{\text{Number of seeds put for germination}} \times 100$$

**Radical Length:** Ten seedlings were selected randomly from each treatment on 14<sup>th</sup> day from germination test. The radical length was measured from the tip of the primary root to base of hypocotyls with the help of a scale and mean radical length was expressed in centimeters.

**Plumule Length:** Ten random seedlings from each genotype were used for taking observation on plumule length. The plumule length was measured from the tip of the primary leaf to the base of the epicotyl and mean plumule length was expressed in centimeter.

**Radical Plumule Ratio:** Radical plumule ratio was worked out by using the following formula

$$R/P \text{ ratio} = \text{mean length of the radical (cm)} / \text{mean length of plumule (cm)}.$$

The mean data of each character was subjected to statistical analysis for variance and test the significance of each character as per the procedure of **Panse and Sukhatme (1967)**. The genotypic coefficient variation (GCV) and phenotypic coefficient (PCV) of variation were calculated by the formulae given by **Burton (1952)**. Heritability in broad sense [ $h^2(\text{bs})$ ] and genetic advance (GA) were estimated as per the method given by **Johnson *et al.* (1955)**.



**Plate 1: Variability in Seed Germination in Some Rice Genotypes Under Study**



**Plate 2: Variability in Root Shoot Development in Some Rice Genotypes 14 DAP**



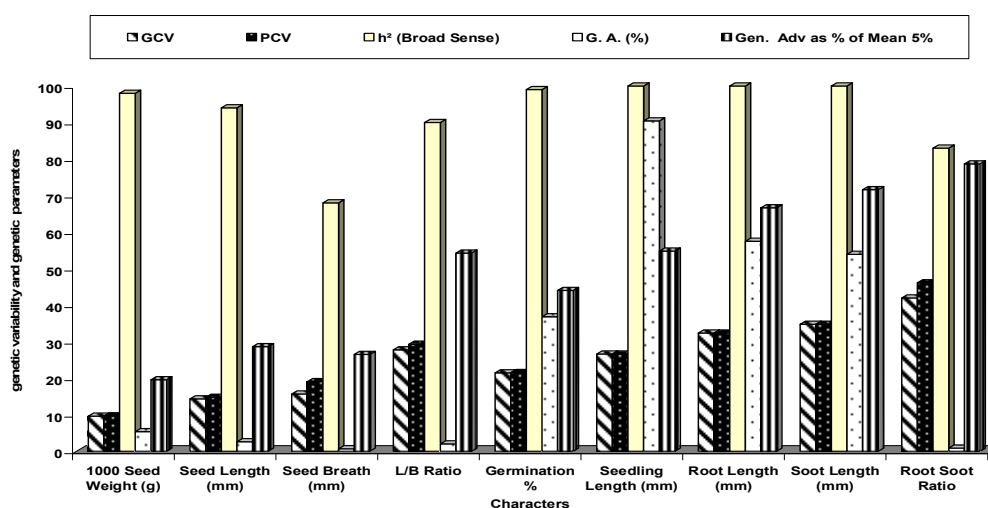
**Plate 3: Variability in Shoot Length 14DAP**

\*DAP = Days after plating

## RESULTS AND DISCUSSIONS

**Morphological traits: Mean performance of all** characters showed the presence of a considerable level of variability. The high coefficient of variation (CV) was exhibited by the trait radical:plumule ratio (12.11%) followed by seed breadth (10.85%) while as lowest value of coefficient of variation was exhibited by seedling length (0.19%). (Plate 1, 2 &3)

Phenotypic coefficient of variation is higher than genotypic coefficient of variation for all the traits (figure 1). Highest value of phenotypic coefficient of variation (PCV) 46.11 and genotypic coefficient of variation (GCV) 41.97 was observed in character radical plumule ratio followed by Plumule length (34.76 and 34.77) and 1000 seed weight showed lowest (9.67) value of phenotypic coefficient of variation and genotypic coefficient of variation (9.59). Highest (100%) magnitude of broad sense heritability was exhibited by seedling length and radical length (100%) while as lowest (68%) was exhibited by seed breadth. Highest value (90.43) of genetic advance was exhibited by seedling length followed by radical length (57.47) and plumule length (53.90), while as lowest value (0.68) of genetic advance was exhibited by seed breadth. However, highest genetic advance as percentage of mean (78.67) was exhibited by radical plumule ratio followed by radical (71.61) and plumule length (66.64) while as lowest value exhibited by the character 1000 seed weight *i.e* 19.58.



**Figure 1: Estimation of Genetic Variability and Genetic Parameters for Different Characters in Rice *Oryza sativa* L.**

### Cluster Analysis

On the basis of agronomic and morphologic characters the unweighted pair group method using arithmetic averages (UPGMA) is most commonly used (Mohammadi and Prasanna, 2003). All thirty five genotypes in this study were grouped into six clusters based on hierarchical clustering (table 1, Figure 2 & 3) cluster I comprises of five genotypes, cluster II consists of fourteen genotypes, cluster III consists of twelve genotypes, cluster IV consists of only one genotype, cluster V consists of one genotype, cluster VI consists of two genotypes. Group V genotypes had maximum germination percentage of 214.39. The clustering difference of some clusters indicate that the genetic diversity found among the genotypes belonging to same geographical origin and might be due to differences in adaptation, selection criteria, selection pressure, and environmental condition (Vivekanandan and Subramanian, 1993; Nayak et al., 2004)

Table 1: Distribution of the Thirty Five Genotypes of Rice into Different Clusters

S. No	Cluster Numbers	Number of Genotypes	Genotypes Included
1	I	5	SR-3, CH-972, SKAU-98, CH-1007, SKAU-46
2	II	14	CH-1039, K-1416-14-3, SR-2, SK-419, Heera, PS-5, PS-1509, SK-423, K-1329-10-4, K-1416-23-5, Jehlum, VL-DHAN-4932, K-1416-26-2, VL DHAN-7314
3	III	12	K-1329-16-3, SK-410, K-1331-3-1, SK-408, K-332, K-1416-8-1, SK-337, K-1313-24-3, K-1331-1-2, SR-1, K-1356-6-4, CH-988
4	IV	1	K-1313-51-3
5	V	1	K-1416-20-2
6	VI	2	SK-420 and PS-3

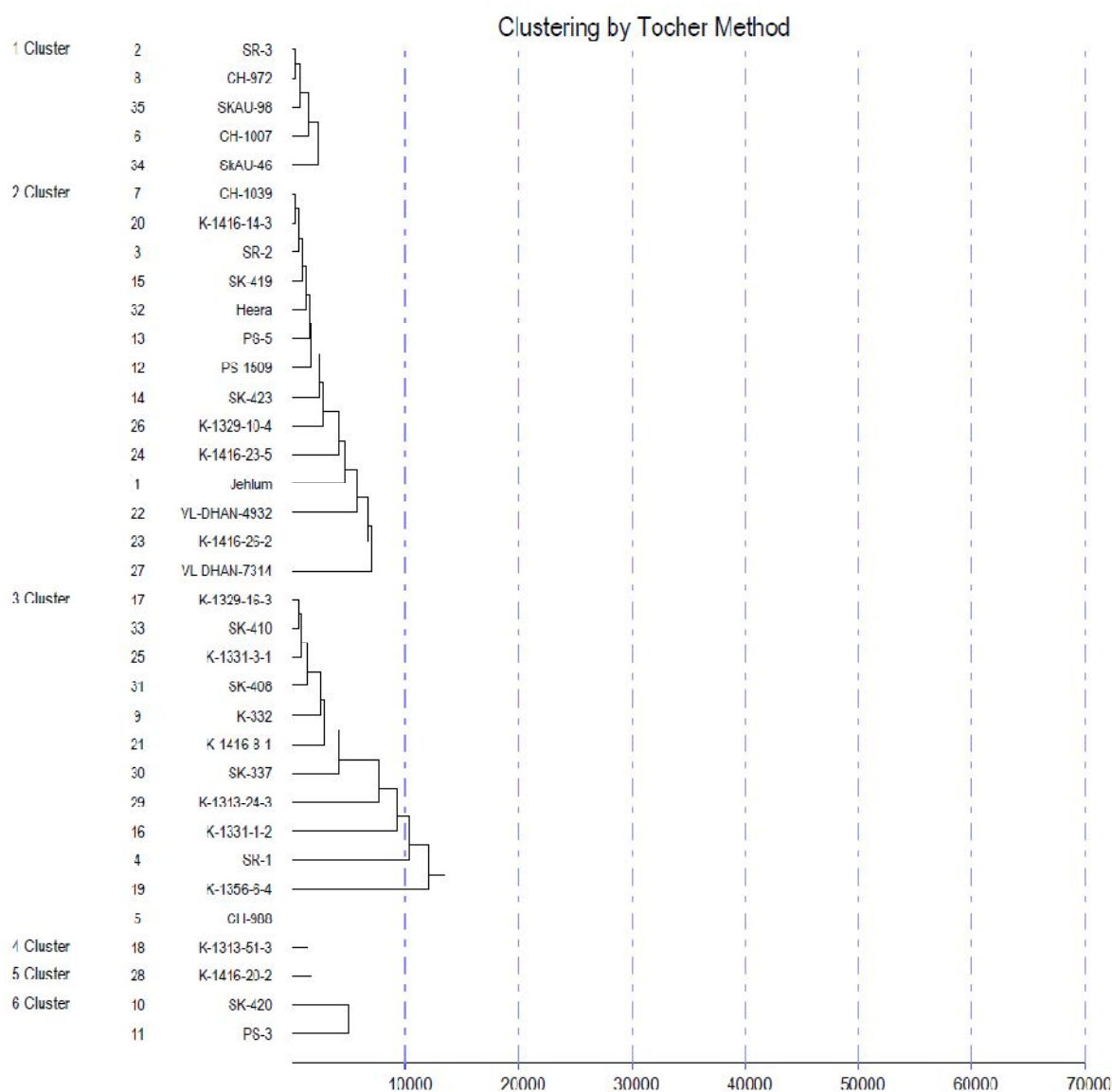
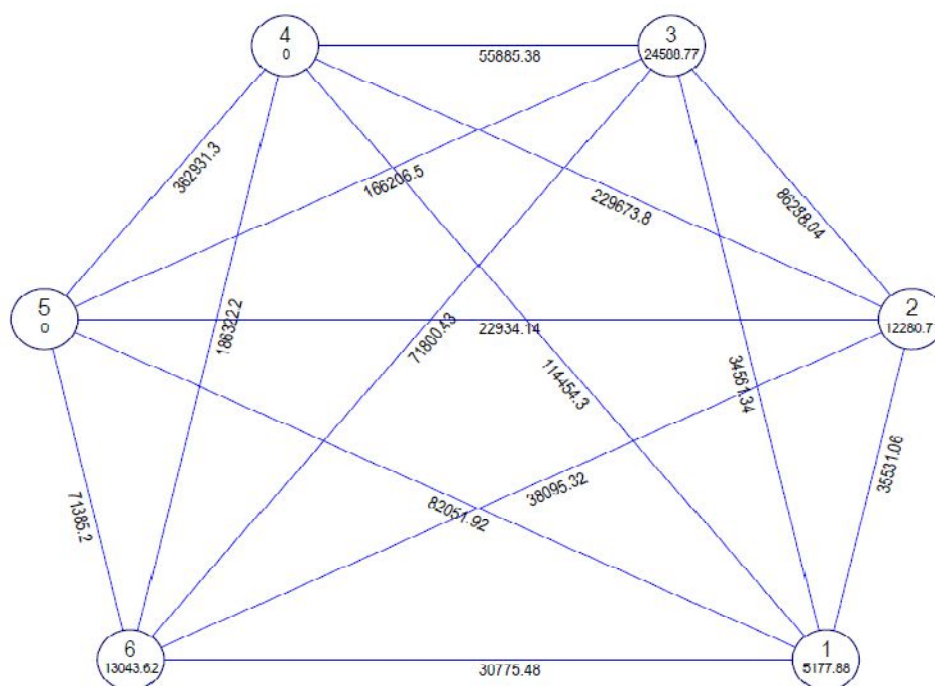


Figure 2: Distribution of the Thirty Five Genotypes of Rice into Different Clusters



## Tocher Method

**Mahalanobis Euclidean Distance (Not to the Scale)****Figure 3: Mahalanobis Euclidean Distance****Intra and Inter Cluster Distance**

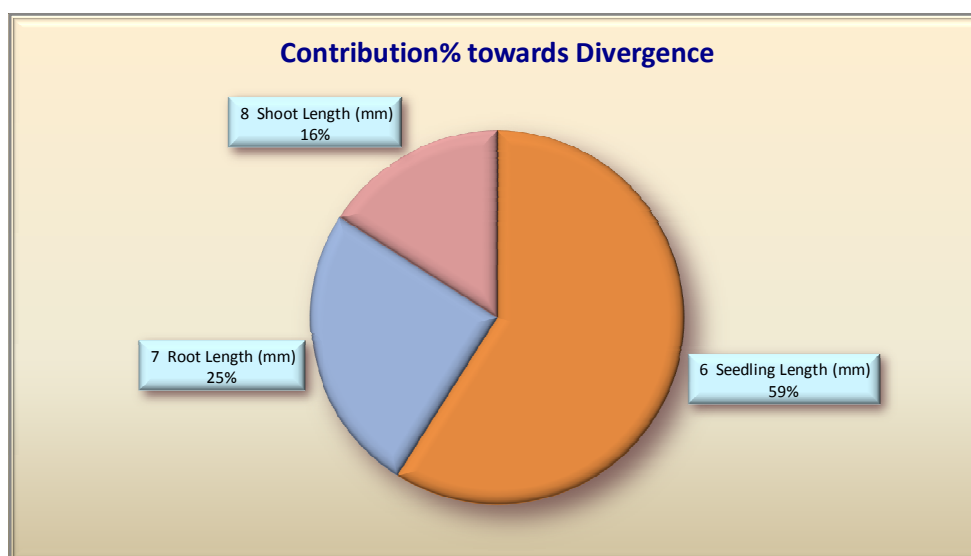
The intra and inter-cluster value in terms of  $D^2$  value among the six clusters are given in table 2. The intra-cluster  $D^2$  values showed that cluster IV (39890.34) had the maximum genetic diversity followed by cluster III (39130.84). The inter-cluster  $D^2$  values of the six clusters showed that the highest inter-cluster  $D^2$  value was between cluster VI and II (646649.40) whereas, the lowest was between cluster II and II (21385.84). From the above, it is concluded that the inter cluster distance in almost all of the clusters was larger than intra cluster distance indicating that wider diversity is present among the genotypes of different groups. This could be the result of selection in different direction by nature and human. These results are in consonance with the findings of Iftekharuddaula et al. (2002) and Khalequzzaman et al. (2008) in rice. To realize much variability and high heterotic effect, parents should be taken from two clusters having wider inter-cluster distance also suggested by Saini and Kaiker, (1987), Mishra et al. (2004) and Chaturvedi and Maurya (2005).

**Table 2: Intra (Diagonal) and Inter Cluster Average Distances ( $D^2$ ) for Different Quantitative Characters in Rice**

	I	II	III	IV	V	VI
I	<b>23918.1</b>	59022.36	122353.4	171283.5	136061.5	480157.200
II		<b>21385.84</b>	120004.2	186720.5	244723.3	646649.400
III			<b>39130.84</b>	128918.4	172961.5	454445.700
IV				<b>39890.34</b>	90236.07	222452.700
V					<b>24892.14</b>	136064.800
VI						<b>28177.740</b>

### Percent Contribution of Each Character to Total Divergence

The number of times that each component appeared in first rank and its respective contribution towards genetic divergence is presented in Figure 4. The results showed that the contribution of seedling length towards genetic divergence was highest (58.99) by taking 351 times ranking first, followed by radical length (25.04) by 149 times and plumule length (15.97) by 95 times. Thousand seed weight, seed length, seed breadth, L/B ratio, germination percentage, radical to plumule ratio did not contribute towards genetic divergence among the genotypes under investigation. However, mean difference among the genotypes is relatively low as most of the genotypes were originated from almost similar climatic conditions. These results were supported by the findings of Choudhary et al. (1999) and Ahmad et al. (2010).



**Figure 4: Percent Contribution of Different Quantitative Characters Towards Genetic Divergence in Rice Genotypes**

### Cluster Mean

The mean value of nine characters studied in thirty genotypes for six clusters is presented in table 3. The genotypes of cluster II (25.71) exhibited the lowest value of 1000 grain weight, whereas, genotypes of cluster VI (29.45) exhibited the highest value of 1000 grain weight, while as others show medium value for 1000 seed weight. The genotypes of cluster III (10.30) exhibited highest value of seed length whereas, genotypes of cluster I (7.90) exhibited lowest value of seed length. The genotypes of cluster VI (3.35) exhibited highest value of seed breadth, whereas, genotypes of cluster III (2.20) exhibited lowest value of seed breadth. The genotypes of cluster III (4.72) exhibited highest value of L/B ratio, whereas, genotypes of cluster I (2.84) exhibited lowest value of L/B ratio. The genotypes of cluster I (99.73) exhibited highest value of germination percentage, whereas genotypes of cluster III (72.39) exhibited lowest value. The genotypes of cluster V (214.39) exhibited highest value of seedling length, where as genotypes of cluster III (108.40) exhibited lowest value of seedling length. The genotypes of cluster V (127.60) exhibited highest value of radical length, where as genotypes of cluster III (52.52) exhibited lowest value of radical length. The genotypes of cluster I (101.87) exhibited highest value of plumule length, where as genotypes of cluster II (46.30) exhibited lowest value of plumule length. The genotypes of cluster II (1.60) exhibited highest value of radical/ plumule ratio, whereas, genotypes of cluster IV (0.73) exhibited lowest value of radical /plumule ratio.

Table 3: Cluster mean values of six clusters for different quantitative characters in Rice

Clusters Characters	I	II	III	IV	V	VI	Mean
1000 Seed Weight (g)	27.27	25.71	27.30	27.08	27.30	29.45	27.35
Seed Length (mm)	7.90	10.08	10.30	9.34	8.16	8.83	9.10
Seed Breadth (mm)	2.87	2.45	2.20	2.46	2.95	3.50	2.74
L/B Ratio	2.84	4.29	4.72	3.47	2.95	3.50	3.63
Germination (%)	99.73	81.28	72.39	79.25	83.70	85.82	83.70
Seedling Length (mm)	189.00	131.99	108.40	141.42	214.39	196.25	163.58
Radical Length (mm)	82.47	80.15	52.52	61.21	127.60	102.64	84.43
Plumule Length (mm)	101.87	46.30	58.54	75.52	85.71	88.22	76.03
Radical/plumule Ratio	0.77	1.60	0.77	0.73	1.35	1.17	1.07

The above grouping indicates the existence of broad genetic divergence among present genotypes. These observations suggest that inter crossing of genotypes from different cluster showing good mean performance may help in obtaining high yielding and good quality genotypes.

## CONCLUSIONS

The present study showed the existence of a considerable amount of diversity among the thirty five elite genotypes of rice. High values of heritability recorded for Plumule length, radical length, seedling length 1000 seed weight and L/B ratio shows that these traits can be successfully transferred to develop desirable genotypes. The traits seedling length, radical and plumule length showed high amount of genetic advance which implies that these characters could be used to select genotypes for changing climatic conditions. For most of the traits significant difference among genotypes were disclosed by cluster analysis and presence of diversity among rice genotypes it is concluded that by keeping in view the clustering distance breeders can use these genotypes for developing new cultivars. Hence, the results will be of greater importance to identify parents for improving various morphological traits analyzed in this study.

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